

FEATURES		Location/Qualifiers	
source	1..4321	/organism="synthetic construct"	
BASE COUNT	966 a 1281 c 1168 g 906 t		
ORIGIN			
Query Match	82.4%;	Score 4188.2;	DB 6; Length 4321;
Best Local Similarity	99.1%;	Pred. No. 0;	
Matches 4297;	Conservative	0; Mismatches	16; Indels 24; Gaps 8;
QY	754	CGAGATCCCGGAGCGCAGCTTGTGGAGAGCGGGAACCGTCCGGAGCAGCCAGAGG	813
Db	1	CGAGATCCCGGAGCGCAGCTTGTCTGGAGAGCGGG-ACGGTCCGGAGCAGCCACAGG	59
QY	814	CAGAGGAGCGCAGAGAGGAAAGAGCCNAGCTAGCCGCTCCAGTGTGTACAGNAGC	873
Db	60	CAGAGGAGCGCAGAGAGGAAAGAGG-CCGAGCTAGCCGCTCCAGTGTGTACAGGAGC	118
QY	874	CGAA-GGACGACACCGCAGCCCGCAGCCCGGCTCCAGCAGCAGCNAAGCGCTTGA-	931
Db	119	CGAAGGAGCAGCACACCGCAGCCCGCAGCCCGGCTCCAGCAGCAGCNAAGCGCTTGA	178
QY	932	-----NCGGTTTCGAAAGCGCGCCCGGAGCTGCCCTTCTCTTCGGTGAAGTTTTAAA	986
Db	179	CGCGGCGGCTTCGAAGCGCGCGCCCGGAGCTGCCCTTCTCTTCGGTGAAGTTTTAAA	238
QY	987	AGCTGCTAAAGACTTCGGAGGAAAGCAAGAAAGTGCCTGTAGACTGAGCGGTGCTTTG	1046
Db	239	AGCTGCTAAAGACTTCGGAGGAAAGCAAGAAAGTGCCTGTAGACTGAGCGGTGCTTTG	298
QY	1047	TCCTCTCTCTTCACCCCGGCTCCGCCAGCCTGCTTCCGCCCTCCGCCCTCCGCCCTCTC	1106
Db	299	TCCTCTCTCTTCACCCCGGCTCCGCCAGCCTGCTTCCGCCCTCCGCCCTCCGCCCTCTC	358
QY	1107	TCCCGCAGCTGCCTCAGTCGGTACTCTCAGCCAAACCCCTCCACACCTTCTCCCCAC	1166
Db	359	TCCCGCAGCTGCCTCAGTCGGTACTCTCAGCCAAACCCCTCCACACCTTCTCCCCAC	418
QY	1167	CGCGCCCGCCCGCCCGCTGGCGCCAGCGTNCAGNCGAGTTTGCAGAGAGTAACTCC	1226
Db	419	CGCGCCCGCCCGCCCGCTGGCGCCAGCGCTGCCAGCCCGAGTTTGCAGAGAGTAACTCC	478
QY	1227	CTTTGGCTCGCAGCGGCGAGNCTAGCTGCACATTGCAAGAGAGGCTCTTAGAG-CAAG	1285
Db	479	CTTTGGCTCGCAGCGGCGAG-CTAGCTGCACATTGCAAGAGAGGCTCTTAGAGCCAGG	537
QY	1286	CGACTGGGAGCGGCTTCAGCACTGCAGCCAGCAGCCGCTGTAGGCTGCACGCGGAG	1345
Db	538	CGACTGGGAGCGGCTTCAGCACTGCAGCCAGCAGCCGCTGTAGGCTGCACGCGGAG	597
QY	1346	AGAACCTCTGTTTCCCGCCTCTCTCCACCTCTCTCCCTGCTCCCGCCCGCGAGTG	1405
Db	598	AGAACCTCTGTTTCCCGCCTCTCTCTCCACCTCTCTCCCTGCTCCCGCCCGCGAGTG	657
QY	1406	CGGAGCCAGAGATCAAAAGATGAAAGGAGTCAAGTCTTCTAGTAGCCAAACAAAC	1465
Db	658	CGGAG-CAGAGATCAAAAGATGAAAGGAGTCAAGTCTTCTAGTAGCCAAACAAAC	716
QY	1466	AAACAAACAAACAAACGCGAAATAAAGAAAGATATAACTCAGTCTTATTTCAC	1525
Db	717	AAACAAACAAACAAACGCGAAATAAAGAAAGATATAACTCAGTCTTATTTCAC	776
QY	1526	CTACTTCAGTGGACACTGAATTTGGAAGTGGAGAGTTTGTTCCTTTTAAAGATCT	1585
Db	777	CTACTTCAGTGGACACTGAATTTGGAAGTGGAGAGTTTGTTCCTTTTAAAGATCT	836
QY	1586	GGCAGCTTTTGAATCTACCTTCAGATTAAGAGACAGACTGTGAGCCTTAGCAGGGCA	1645
Db	837	GGGATCTTTTGAATCTACCTTCAGATTAAGAGACAGACTGTGAGCCTTAGCAGGGCA	896
QY	1646	GATCTTGTCACCGGTGCTTCTTCGACGAGACTTTGAGGCTGTACAGAGCGCTTTT	1705

Db	897	GATCTTGTCACCGCTGTCTTCTTCTGACGAGACTTTGAGGCTGTACAGCGCTTTT	956
QY	1706	GCSTGTTGTTCCCGCAAGTTTCTTCTTGGAGCTTCCCGCAGGTGGGAGCTAGTGTG	1765
Db	957	GCSTGTTGTTCCCGCAAGTTTCTTCTTGGAGCTTCCCGCAGGTGGGAGCTAGTGTG	1016
QY	1766	AGCGACTACCGCATCATCACAGCCTGTTGAACCTTCTTGTAGCAAGAGAGGGAGCGG	1825
Db	1017	AGCGACTACCGCATCATCACAGCCTGTTGAACCTTCTTGTAGCAAGAGAGGGAGCGG	1076
QY	1826	GTAAAGGAAGTAGTGGAAAGATTTCAGCCAAAGCTCAAGATGGAAGTGTAGGGCTGG	1885
Db	1077	GTAAAGGAAGTAGTGGAAAGATTTCAGCCAAAGCTCAAGATGGAAGTGTAGGGCTGG	1136
QY	1886	GAAGGTCTTACCTTCGGCCGCGTCCAAGACTTACCGAGGAGCTTTCAGAAATCTGTTC	1945
Db	1137	GAAGGTCTTACCTTCGGCCGCGTCCAAGACTTACCGAGGAGCTTTCAGAAATCTGTTC	1196
QY	1946	AGAGCGTGGCGAAGTGTATCCAGAACCCGGGCCCCAGACCCAGAGCGCGAGCGCAG	2005
Db	1197	AGAGCGTGGCGAAGTGTATCCAGAACCCGGGCCCCAGAGCCAGAGCGCGAGCGCAG	1256
QY	2006	CACCTCCCGCGCCAGTTTGTCTGCTGCTGACGACGACGACGACGACGACGACGACG	2065
Db	1257	CACCTCCCGCGCCAGTTTGTCTGCT-----GCAGCAGCAGCAGCAGCAGCAGCAGC	1304
QY	2066	AGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG	2125
Db	1305	AGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG	1364
QY	2126	AGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG	2185
Db	1365	AGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG	1424
QY	2186	GCTACCTGTGCTGTGGATGAGGAACAGCAACCTTCACAGCGCAGTTCGCGCCCTGGAGTGC	2245
Db	1425	GCTACCTGTGCTGTGGATGAGGAACAGCAACCTTCACAGCGCAGTTCGCGCCCTGGAGTGC	1484
QY	2246	ACCCGAGAGAGTTCGCTCCAGAGCCTCCCGAGCAGGATGACTCAGCTGCCCTCCCTCCAGCTTGTCCC	2365
Db	1485	ACCCGAGAGAGTTCGCTCCAGAGCCTCCCGAGCAGGATGACTCAGCTGCCCTCCCTCCAGCTTGTCCC	1544
QY	2306	CGCAGCAGCTGCCAGCAGCTCCCGAGCAGGATGACTCAGCTGCCCTCCCTCCAGCTTGTCCC	2365
Db	1545	CGCAGCAGCTGCCAGCAGCTCCCGAGCAGGATGACTCAGCTGCCCTCCCTCCAGCTTGTCCC	1604
QY	2366	TGCTGGGCCCCACTTTCGCCGCTTAAAGCAGCTGCTCCGCTGACCTTAAAGACATCTCTGA	2425
Db	1605	TGCTGGGCCCCACTTTCGCCGCTTAAAGCAGCTGCTCCGCTGACCTTAAAGACATCTCTGA	1664
QY	2426	CGGAGGCGCAGCAGCATGCAACTCTTTCAGCAACAGCAGCAGGAGCAGTATCCGAAAGCA	2485
Db	1665	CGGAGGCGCAGCAGCATGCAACTCTTTCAGCAACAGCAGCAGGAGCAGTATCCGAAAGCA	1724
QY	2486	GCAGCAGCGGGAGAGCGAGGAGGCGCTTCGGGCTCCCACTTCTCCCAAGGACAATTAAT	2545
Db	1725	GCAGCAGCGGGAGAGCGAGGAGGCGCTTCGGGCTTCCTTCTCCCAAGGACAATTAAT	1784
QY	2546	TAGGGGCACTTCGACCACTTCTGACAAACCCCAAGGAGTGTGTAAAGCAGTGTGCGGTGT	2605
Db	1785	TAGGGGCACTTCGACCACTTCTGACAAACCCCAAGGAGTGTGTAAAGCAGTGTGCGGTGT	1844
QY	2606	CCATGGGCTGGGTGTGAGGCGTTCAGTCATCTGAGTCCAGGGGAAACAGCTTCGGGGGG	2665
Db	1845	CCATGGGCTGGGTGTGAGGCGTTCAGTCATCTGAGTCCAGGGGAAACAGCTTCGGGGGG	1904
QY	2666	ATTGCACTAGCGCCCACTTTTGGGAGTTCACCCGCTGTGCGTCCCTCTTGTGCC	2725
Db	1905	ATTGCACTAGCGCCCACTTTTGGGAGTTCACCCGCTGTGCGTCCCTCTTGTGCC	1964
QY	2726	CATTGGCCGAATGCAAGGTTCTCTGCTAGACGACAGCGCAGGCAAGCAGCTGAAGATA	2785
Db	1965	CATTGGCCGAATGCAAGGTTCTCTGCTAGACGACAGCGCAGGCAAGCAGCTGAAGATA	2024

QY	2786	CTGCTGAGTATCCCTTTCAAGGGAGGTTACACCAAGGGCTAGAAAGCGGAGACCCCTAG	2845
Db	2025	CTGCTGAGTATCCCTTTCAAGGGAGGTTACACCAAGGGCTAGAAAGCGGAGACCCCTAG	2084
QY	2846	GCTGCTCTGGCAGCGCTGCACAGGGAGCTCCGGGACACTTGAATGCGCGTCTACCCCTGT	2905
Db	2085	GCTGCTCTGGCAGCGCTGCACAGGGAGCTCCGGGACACTTGAATGCGCGTCTACCCCTGT	2144
QY	2906	CTCTCTACAAGTCCGGAGCACTGGACGAGGACGTCGCTACAGAGTCCGCACTACTACAA	2965
Db	2145	CTCTCTACAAGTCCGGAGCACTGGACGAGGACGTCGCTACAGAGTCCGCACTACTACAA	2204
QY	2966	ACTTTCCACTGCTCTGCGCGGACGCCGCCCTCCGCCGCTCCCATCCCCACGCTC	3025
Db	2205	ACTTTCCACTGCTCTGCGCGGACGCCGCCCTCCGCCGCTCCCATCCCCACGCTC	2264
QY	3026	GCATCAAGCTGGAAACCGCTGGACTACGGCAGCGCTTGGCGGCTGCGCGCGCGAGT	3085
Db	2265	GCATCAAGCTGGAAACCGCTGGACTACGGCAGCGCTTGGCGGCTGCGCGCGCGAGT	2324
QY	3086	GCGGCTATGGGACCTGGCGAGCGCTGCATGGCGGGGTGCAGCGGGACCCGGTTCTGGGT	3145
Db	2325	GCGGCTATGGGACCTGGCGAGCGCTGCATGGCGGGGTGCAGCGGGACCCGGTTCTGGGT	2384
QY	3146	CACCTCTAGCCCGCGCTTCTCATCTGSCACACTCTCTTACACAGCCGAAAGGCCAGT	3205
Db	2385	CACCTCTAGCCCGCGCTTCTCATCTGSCACACTCTCTTACACAGCCGAAAGGCCAGT	2444
QY	3206	TGATATGACCGCTGTGTGTGTGGGGTGTGTGGCGCGGGCGCGCGCGCGCGCGG	3265
Db	2445	TGATATGACCGCTGTGTGTGTGGGGTGTGTGGCGCGGGCGCGCGCGCGCGCGG	2504
QY	3266	GCGCGCGCGCGCGCGCGCGCGGCGGAGCGGGAGCTGTAGCCCTCTAGCGCTACAGCTC	3325
Db	2505	GCGCGCGCGCGCGCGCGCGCGGCGGAGCGGGAGCTGTAGCCCTCTAGCGCTACAGCTC	2564
QY	3326	GGCCCTCTCAGGGGCTGGCGGGCCAGGAAGGACTTACCGCACTGTGTGTGTGTACC	3385
Db	2565	GGCCCTCTCAGGGGCTGGCGGGCCAGGAAGGACTTACCGCACTGTGTGTGTGTACC	2624
QY	3386	CTGGCGGCATGTTGAGCAGAGTGCCCTATCCAGTCCCACTTGTGTCAAAAGCGAAATGG	3445
Db	2625	CTGGCGGCATGTTGAGCAGAGTGCCCTATCCAGTCCCACTTGTGTCAAAAGCGAAATGG	2684
QY	3446	GCCCTCGATGATAGCTACTCCGACACTTACGGGGACATTCGCTTTGGAGACTGCCAGGG	3505
Db	2685	GCCCTCGATGATAGCTACTCCGACACTTACGGGGACATTCGCTTTGGAGACTGCCAGGG	2744
QY	3506	ACCATGTTTGGCCATTGCACTATTACTTCCACCCAGAGACCTCCCTGATCTGTGGAG	3565
Db	2745	ACCATGTTTGGCCATTGCACTATTACTTCCACCCAGAGACCTCCCTGATCTGTGGAG	2804
QY	3566	ATGAAGCTTCTGGTGTCACTATGGAGCTCTACATGTGGAAGCTGCAAGGCTCTCTTCA	3625
Db	2805	ATGAAGCTTCTGGTGTCACTATGGAGCTCTACATGTGGAAGCTGCAAGGCTCTCTTCA	2864
QY	3626	AAAGAGCCGCTGAAGGGAAACAGAAAGTACCTGTGCGCCAGCAGAAATGATTCGCACTATG	3685
Db	2865	AAAGAGCCGCTGAAGGGAAACAGAAAGTACCTGTGCGCCAGCAGAAATGATTCGCACTATG	2924
QY	3686	ATAAATTCGGAAGGAAAATTTGTCATCTTTGTCGCTTCCGAAATGTTATGAACAGGGA	3745
Db	2925	ATAAATTCGGAAGGAAAATTTGTCATCTTTGTCGCTTCCGAAATGTTATGAACAGGGA	2984
QY	3746	TGACTCTGGAGCCCGGAAGCTGAGAAACTTGGTAATCTGAACTACAGGAGGAAGGAG	3805
Db	2985	TGACTCTGGAGCCCGGAAGCTGAGAAACTTGGTAATCTGAACTACAGGAGGAAGGAG	3044
QY	3806	AGGCTTCCAGCACCAGCCCACTGAGGAGACACCCAGAGCTGACAGTGCACACA	3865
Db	3045	AGGCTTCCAGCACCAGCCCACTGAGGAGACACCCAGAGCTGACAGTGCACACA	3104

QY	3866	TTGAAGGCTATGAATGTACAGCCATCTTTCTCAATGTCTCTGGAAGCCATTTAGCCAGGTG	3925
Db	3105	TTGAAGGCTATGAATGTAGCCCATCTTTCTGAATGTCTCTGGAAGCCATTTAGT	3164
QY	3926	TAGTGTGCTGGACAGACAAACACCCGCGACTCTCTTGCAGCCCTTCTCTCTATGCC	3985
Db	3165	TAGTGTGCTGGACAGACAAACACCCGCGACTCTCTTGCAGCCCTTCTCTCTATGCC	3224
QY	3986	TCAATGAACCTGGAGAGACAGCTGTACAGTGGTCAAGTGGCCGACAGGCTTGGCTG	4045
Db	3225	TCAATGAACCTGGAGAGACAGCTGTACAGTGGTCAAGTGGCCGACAGGCTTGGCTG	3284
QY	4046	GCTTCGGCAACTTACAGTGGAGACAGATGGCTGTCAATTCAGTACTCTCTGGATGGGC	4105
Db	3285	GCTTCGGCAACTTACAGTGGAGACAGATGGCTGTCAATTCAGTACTCTCTGGATGGGC	3344
QY	4106	TCATGGTCTTTGCCATGGCTGGCGATCTCTTACCAATGTCAACTCCAGGATGCTCTACT	4165
Db	3345	TCATGGTCTTTGCCATGGCTGGCGATCTCTTACCAATGTCAACTCCAGGATGCTCTACT	3404
QY	4166	TCGCCCCGTGATCTGGTTTCAATGAGTACCGCATGCAAAAGTCCCGGATGTACAGCCAGT	4225
Db	3405	TCGCCCCGTGATCTGGTTTCAATGAGTACCGCATGCAAAAGTCCCGGATGTACAGCCAGT	3464
QY	4226	GTGTCCGAATGAGCACACTCTCTCAAGAGTTTGGATGGCTCCAAATACCCCCCAGGAAT	4285
Db	3465	GTGTCCGAATGAGCACACTCTCTCAAGAGTTTGGATGGCTCCAAATACCCCCCAGGAAT	3524
QY	4286	TCCGTGTCATGAAGCACTGCTACTCTTCAAGAGTTTGGATGGCTCCAAATACCCCCCAGGAAT	4345
Db	3525	TCCGTGTCATGAAGCACTGCTACTCTTCAAGAGTTTGGATGGCTCCAAATACCCCCCAGGAAT	3584
QY	4346	AAAAATCTTTGATGAATTCGAATGAACATACATCAAGGAACCTCGATCTATCATTTGCAT	4405
Db	3585	AAAAATCTTTGATGAATTCGAATGAACATACATCAAGGAACCTCGATCTATCATTTGCAT	3644
QY	4406	GCAAGAAATCCACATCTCTGCTCAAGAGCTTTACAGAGTACCAAGCTCTCTGG	4465
Db	3645	GCAAGAAATCCACATCTCTGCTCAAGAGCTTTACAGAGTACCAAGCTCTCTGG	3704
QY	4466	ACTCCGTGAGCCTATTGGAGAGAGCTGCATCAGTTCATCTTTCAGCTGTCTTAATCAAGT	4525
Db	3705	ACTCCGTGAGCCTATTGGAGAGAGCTGCATCAGTTCATCTTTCAGCTGTCTTAATCAAGT	3764
QY	4526	CACACATGTGAGCGTGGACTTTCGGAAATGATGCGAGAGATCATCTCTGTGCAAGTGC	4585
Db	3765	CACACATGTGAGCGTGGACTTTCGGAAATGATGCGAGAGATCATCTCTGTGCAAGTGC	3824
QY	4586	CCAAGATCTTTCTGSGAAAGTCAAGCCCATCTATTCCACACCCAGTGAAGCATTTGAA	4645
Db	3825	CCAAGATCTTTCTGSGAAAGTCAAGCCCATCTATTCCACACCCAGTGAAGCATTTGAA	3884
QY	4646	ACCCATTTCCACCCAGCTCATGCCCCCTTTTCAGATGTCTTGCTGCTCTTAATCACT	4705
Db	3885	ACCCATTTCCACCCAGCTCATGCCCCCTTTTCAGATGTCTTGCTGCTCTTAATCACT	3944
QY	4706	TGCACTACTCTCTCAGTGGCTTGGGAAATTCCTCTATTGATGTACAGTCTGTCAATGA	4765
Db	3945	TGCACTACTCTCTCAGTGGCTTGGGAAATTCCTCTATTGATGTACAGTCTGTCAATGA	4004
QY	4766	ACATGTCTCTGAATTCATTTGCTGGGCTTTTTTTTCTCTTCTCTCTCTCTCTCTCTCT	4825
Db	4005	ACATGTCTCTGAATTCATTTGCTGGGCTTTTTTTTCTCTCTCTCTCTCTCTCTCTCTCT	4064
QY	4826	TCTTCCCTCCCTATCTAACCTCCCATGGACCTTCAGACTTTGCTTCCCATTTGGCTC	4885
Db	4065	TCTTCCCTCCCTATCTAACCTCCCATGGACCTTCAGACTTTGCTTCCCATTTGGCTC	4124
QY	4886	CTATCTGTGTTTGAATGGTGTATGTCCTTTAAATCTGTGATGATCTCATATGGCCC	4945
Db	4125	CTATCTGTGTTTGAATGGTGTATGTCCTTTAAATCTGTGATGATCTCATATGGCCC	4184
QY	4946	AGTGTCAAGTGTGCTTTTACAGCACTACTCTGTGCCAGCACACAACGTTTACTTTA	5005

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Db 4185 AGTGCAAGTTGTTGTTTACAGCACTACTGTGCGCAGCCACACAAAGCTTACTTA 4244
QY 5006 TCTTATGCCACGGGAAGTTTATAGAGCTAAGATTATCTGGGGAATCAAAACAAAAACA 5065
Db 4245 TCTATGCCACGGGAAGTTTATAGAGCTAAGATTATCTGGGGAATCAAAACAAAAACA 4304
QY 5066 AGCAACAAAAA 5082
Db 4305 AGCAACAAAAA 4321

RESULT 2
AR153576 3715 bp DNA linear PAT 08-AUG-2001
LOCUS Sequence 10 from patent US 6235872.
DEFINITION AR153576
ACCESSION AR153576
VERSION AR153576.1 GI:15121108
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 3715)
AUTHORS Bredesen, D.E. and Rabinzadeh, S.
TITLE Proapoptotic peptides dependence polypeptides and methods of use
JOURNAL Patent: US 6235872-A 10 22-MAY-2001;
FEATURES
source Location/Qualifiers
1..3715
BASE COUNT 841 a 1055 c 1001 g 818 t
ORIGIN

Query Match 70.8%; Score 3595.8; DB 6; Length 3715;
Best Local Similarity 98.6%; Pred. No. 0;
Matches 3685; Conservative 0; Mismatches 7; Indels 45; Gaps 4;

QY 1335 TCCAGCGGAGAGACCTCTGTTTCCCGCACTCTCTCTCCACCTCCCTCCCTGCTTCCC 1394
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QY 1395 CACCCCGAGTGGGAGCAGAGATCAAAAGATGAAAGGAGTCAGTCTTCAGTAGCCA 1454
Db 64 CACCCCGAGTGGGAG -CAGAGATCAAAAGATGAAAGGAGTCAGTCTTCAGTAGCCA 122
QY 1455 AAAACAAACAAACAAACAAACAAACAAACAAACAAACAAACAAACAAACAAACAAAC 1514
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Db 183 CTATTGTCACCTACTTTCAGTGGACACTGAATTTGGAAGTGGAGGATTTGTTTTC 242
QY 1575 TTTTAGATCTGGGATCTTTTGAATCTACCTTCAAGTATTAAGACAGACTGTGAGC 1634
Db 243 TTTTAGATCTGGGATCTTTTGAATCTACCTTCAAGTATTAAGACAGACTGTGAGC 302
QY 1635 CTAGCAGGCGAGATCTTGTCACCTGTCTCTTCTTCGACGAGACTTTGAGGCTGCA 1694
Db 303 CTAGCAGGCGAGATCTTGTCACCTGTCTCTTCTTCGACGAGACTTTGAGGCTGCA 362
QY 1695 GAGCGTTTTGGTGGTCTCCCGCAGTTTCTCTCTGAGCTTCCCGCAGGTGGG 1754
Db 363 GAGCGTTTTGGTGGTGGTCTCCCGCAGTTTCTCTCTGAGCTTCCCGCAGGTGGG 422
QY 1755 CAGTAGCTCAGCGACTACCGCATCATCAGCGCTGTGTAACCTCTTCGACGAGAA 1814
Db 423 CAGTAGCTCAGCGACTACCGCATCATCAGCGCTGTGTAACCTCTTCGACGAGAA 482
QY 1815 GGGAGGCGGGGTAGGGAAGTAGGTGGAAGATTAGCCAAAGCTCAAGGATGGAAGTCA 1874
Db 483 GGGAGGCGGGGTAGGGAAGTAGGTGGAAGATTAGCCAAAGCTCAAGGATGGAAGTCA 542
QY 1875 GTTAGGCTGGGAAGGCTCTACCTTCGCGCGCGTCCACAGACCTACCGGAGGCTTTTCCA 1934
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Db 543 GTTAGGCTGGGAAGGTTCTACCTCGCGCGCTCCAAGACCTACCGAGGAGCTTTCCA 602
QY 1935 GAATCTGTTCAGAGCTGCGCGAAGTGAATCCAGAACCGGGCCCGAGGACCCAGAGGC 1994
Db 603 GAATCTGTTCAGAGCTGCGCGAAGTGAATCCAGAACCGGGCCCGAGGACCCAGAGGC 662
QY 1995 CGCAGCGCAGACCTCCCGCGCGCAGTTTGTCTGCTCTGCAGCAGCAGCAGCAGCA 2054
Db 663 CGCAGCGCAGACCTCCCGCGCGCAGTTTGTCTGCTCTGCTCTGCTCTGCTCTGCT 701
QY 2055 GCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 2114
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QY 2595 AGTGTGCGTGTCCATGGGCGTGGTGTGGAGCGTTGGAGCATCTGAGTCCAGGGAACA 2654
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QY 2655 GCTTCGGGGGATTCGATGTACGCCCCACTTTTGGGAGTTTCCACCGCTGTGCTCCAC 2714
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QY 2715 TCCTTGTGCCCATTTGCCGGAATCAAAAGTTCTCTCTAGACGACAGCAGCAGCAAGAG 2774
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QY 2775 CACTCAAGATCTGCTGAGTATTCCTCTTCAAGGAGGTTTACACCAAGGCTTAGAAG 2834
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QY 2835 CGAGAGCCTTAGCTGCTCTGCGAGCGCTGAGCAGGAGGCTCCGGGACCTTGAAGTCC 2894
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QY 2895 GTCTACCTGTCTCTCAAGTCCGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 2954
Db 1539 GTCTACCTGTCTCTCAAGTCCGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 1598
QY 2955 CGACTACTAACTTTTCCACTGGCTCTGGCGGAGCGCGCGCTCCGCGCGCTCCCA 3014
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[illegible]

QY	4086	TCAGTACTCCTGGATGGGGCTCATGGTGTGTTGGCATGGGTGGCGATCCTTCCACCAATGT	4145
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QY	4146	CAACTCCAGGATGCTCTACTTTCGCCCTGATCTGGTGTTCATAGAGTACCCGATGCACAA	4205
Db	2799	CAACTCCAGGATGCTCTACTTTCGCCCTGATCTGGTGTTCATAGAGTACCCGATGCACAA	2858
QY	4206	GTTCCGGATGTACAGCCAGTGTGTCCGAATGAGCCACCTCTCTCAAGAGTTTGGATGGCT	4265
Db	2859	GTTCCGGATGTACAGCCAGTGTGTCCGAATGAGCCACCTCTCTCAAGAGTTTGGATGGCT	2918
QY	4266	CCAAATCACCCCCCAGAGAAATTCCTGTGCATGAAGCAGTGTCTTTCAGCATTTATTC	4325
Db	2919	CCAAATCACCCCCCAGAGAAATTCCTGTGCATGAAGCAGTGTCTTTCAGCATTTATTC	2978
QY	4326	AGTGGATGGGCTGAAAAATCAAAAATCTTTGATGAACCTCGAATGAACACTACATCAAGGA	4385
Db	2979	AGTGGATGGGCTGAAAAATCAAAAATCTTTGATGAACCTCGAATGAACACTACATCAAGGA	3038
QY	4386	ACTCGATCGTATCATTCGATGCAAAAAGAAAAATCCACATTCCTGTCTCAAGAGCTTCTA	4445
Db	3039	ACTCGATCGTATCATTCGATGCAAAAAGAAAAATCCACATTCCTGTCTCAAGAGCTTCTA	3098
QY	4446	CCAGCTCACCAAGCTCCTGGACTCCGTGAGCGCTATTGCGAGAGAGCTGATCATGTTCCAC	4505
Db	3099	CCAGCTCACCAAGCTCCTGGACTCCGTGAGCGCTATTGCGAGAGAGCTGATCATGTTCCAC	3158
QY	4506	TTTTTGACCTGCTAATCAAGTTCACACATGCTGAGCGTGACATTCGCGAAATGATGCGAGA	4565
Db	3159	TTTTTGACCTGCTAATCAAGTTCACACATGCTGAGCGTGACATTCGCGAAATGATGCGAGA	3218
QY	4566	GATCATCTCTGTGCAAGTCCCAAGATCCTTTCTGGGAAAGTCAAGCCCATCTATTTCGA	4625
Db	3219	GATCATCTCTGTGCAAGTCCCAAGATCCTTTCTGGGAAAGTCAAGCCCATCTATTTCGA	3278
QY	4626	CACCCAGTGAAGCATTTGGAACCCCTATTTCGCCACCCAGCTCATGCCCCCTTTTCAGATG	4685
Db	3279	CACCCAGTGAAGCATTTGGAACCCCTATTTCGCCACCCAGCTCATGCCCCCTTTTCAGATG	3338
QY	4686	TCTCTCGCTGTATTAACCTCTGCATCTCTCTGCAAGTGCCTTGGGAAATTTCCCTCTAT	4745
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QY	4746	TGATGTACAGTCTGTGCATCAACATGCTTCCGAATCTATTGCTGGGCTTTTTTTTC	4805
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QY	4806	TTTCTCTCCTTTCTTTTCTTTCTTTCCCTCCCTATCTAACCCCTCCCATGGCACCTTCAGAC	4865
Db	3448	TTTCTCTCCTTTCTTTTCTTTCTTTCCCTCCCTATCTAACCCCTCCCATGGCACCTTCAGAC	3507
QY	4866	TTTGTCTCCCATTTGGCTCTACTCTGTTGTTGAAATGGTGTGATGGCTTTTAATCTG	4925
Db	3508	TTTGTCTCCCATTTGGCTCTACTCTGTTGTTGAAATGGTGTGATGGCTTTTAATCTG	3567
QY	4926	TGATGATCCTCATATGGCCCCAGTGTGCTGTTGTTTACAGCAGCTACTCTGTGCCA	4985
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QY	4986	GGCACACAACCTTTACTTATCTTATGCCAGGGAAGTTTAGAGAGCTAAGATATCTGG	5045
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AX409653
LOCUS


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Db 3688 GGAATCAAAACAAAAA 3704
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RESULT 4

LOCUS

HUMARB

DEFINITION

HOMO

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

3715 bp mRNA linear PRI 11-FEB-2002
Homo sapiens androgen receptor (AR) mRNA, complete cds.

M23263.1 GI:178893

androgen receptor; dihydrotestosterone receptor.

Homo sapiens.

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 3715)

Chang, C.S., Kokontis, J. and Liao, S.T.

Structural analysis of complementary DNA and amino acid sequences

of human and rat androgen receptors
Proc Natl Acad Sci U.S.A. 85 (19), 7211-7215 (1988)

Journal	Proc. Natl. Acad. Sci. U.S.A.	Year	Volume	Page	DOI
JOURNAL MEDLINE PUBMED	89017168 31746328	1988 1988	85 7211-7215	1635	10.1073/pnas.85.1635.1639

PUBMED	31/4020
REFERENCE	2 (sites)

REFERENCE
2 (sites)
AUTHORS
Chang, C.S., Kokontis, J. and Liao, S.T.
Molecular cloning of human and rat complementary DNA encoding

TITLE	JOURNAL	DATE	PAGE
Molecular cloning of human and rat androgen receptors	Science	240 (1985)	324-326 (1988)

	DB	363	GAGCGCTTTTTCGTCGTGGTTGGTCCGCCAAGTTTCCTTTCFCGAGACATCCCCCAAGAA	181
			
JOURNAL	Science 240 (4850), 324-326 (1966)			
MEDLINE	88178111			

3353726
Draft entry and computer-readable sequence for [1] kindly provided by S. Liao, 01-MAR-1989.
Four proteins of different sizes were found. These proteins could be explained if alternative start codons at positions 1084, 1252 and 1315 were used.

FEATURES
SOURCE

1. .3715

[illegible][illegible][illegible]

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CDS					

Accession	Gene	Protein	Length
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D00000	product="androgen receptor"	663	

[illegible][illegible][illegible][illegible][illegible][illegible]

819 AGSCCCACAGGCTACCTGTCCTCGGATGAGGAACCAACCTCTACAGCCGCGACG 298

[illegible]

879 CCTGGACTGTCACCCCGAGAGAGGTTGCTCCACAGAGCTGGAGCGCCCGTGGCCGCCAG Db

2295 CANGGGCTCGGACGAGCTGCCAGCAGCTCCGACAGGAGTGAATTCAGCTGCCCCATC
QY

[illegible]

BASE	COUNT	PERCENT	ORIGIN
A	641	100.0	QY
C	1000	156.0	QY
G	1002	156.3	QY
T	999	155.7	QY

Query Match	Similarity	Score	DB	Length
70.8%	98.5%	3595.8	DB	3715
99	99	99	99	99

[illegible]

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1395
Db AGACATCTGACGGAGCCACGACCATGCAACTTTTCAGCAACAGCAGCAGGACAGT 11
1059

db

4 TTTCGGGAGAGAACCCCTGTATTTTCCCCCACTCTCTCACACTCCTCGICGCTTCCC 63

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QV 2475 ATCGAAGCGACGACGCGGGAGACGAGCGGCCCTCGGGGGCTCCCACTCTCTCCAA 25

QY	1395	CACCCCGAGTCGGGAGCCAGAGATCAAAAGATGAAGAATCAGTCTTTCTAGTAGCCA
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QJ	2475	ATCCGAAAGCAGCAGCAGCGGAGAGCGAGGAGGCCTCTGGGGGCTCCCACATTCCTCCAA
D6	1119	ATCCGAAAGCAGCAGCAGCGGAGAGCGAGGAGGCCTCTGGGGGCTCCCACATTCCTCCAA
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ACCESSION 109479
VERSION 109479.1 GI:587808
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 3721)
AUTHORS Liao,S. and Chang,C.-S.
TITLE DNA BINDING PROTEINS INCLUDING ANDROGEN RECEPTOR
JOURNAL Patent: WO 8909223-A 1 05-OCT-1989;
FEATURES Location/Qualifiers
1..3721
/organism="unknown"
BASE COUNT 843 a 1058 c 1004 g 815 t 1 others
ORIGIN
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Best Local Similarity 98.5%; Pred. No. 0;
Matches 3687; Conservative 0; Mismatches 5; Indels 51; Gaps 6;
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Db 702 --GCAG 758
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Db 1179 CTCCAAGGACAAATTTAGGGGCACTTTCAGGCGCACTTCGACCAATTTCTGACACCGCAGGAGTTG 1238
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Db 1239 TAAGCAGTGTGCTGCTCCATGGCGCTGGGTGTGGAGCGCTTGGAGCATCTGACTCCAGG 1298
QY 2649 GGAACAGCTTCGGGGGGAATTCATGTAGCCCACTTTTGGGAGTTCCACCCGCTGTGCG 2708
Db 1299 GGAACAGCTTCGGGGGGAATTCATGTAGCCCACTTTTGGGAGTTCCACCCGCTGTGCG 1358
QY 2709 TCCCACTCTTGTGCGCCCATTTGGCGGAATGCAAGGTTCTCTGTAGACGACGAGCGCAGG 2768
Db 1359 TCCCACTCTTGTGCGCCCATTTGGCGGAATGCAAGGTTCTCTGTAGACGACGAGCGCAGG 1418
QY 2769 CAAGAGCACTGAAGTACTGCTGTAGTATTCCTTTCAGGGAGGTTTACACCAAGGCT 2828
Db 1419 CAAGAGCACTGAAGTACTGCTGTAGTATTCCTTTCAGGGAGGTTTACACCAAGGCT 1478
QY 2829 AGAAGCGGAGAGCTTAGGCTGCTGCGAGCGCTCAGCAGGAGGAGCTCCGGGACACTTGA 2888
Db 1479 AGAAGCGGAGAGCTTAGGCTGCTGCGAGCGCTCAGCAGGAGGAGCTCCGGGACACTTGA 1538
QY 2889 ACTGCCGTCTACCT 2948

Db 1539 ACTGCCGTCTACCTGTCTCTACAAAGTCCGAGACACTGGACGAGGAGCTGCGTACCA 1598
 QY 2949 GAGTCGGGACTACTACAATCTCCACTGCTCTGCGGAGCCGCGCCCTCCGCGCC 3008
 Db 1599 GAGTCGGGACTACTACAATCTCCACTGCTCTGCGGAGCCGCGCCCTCCGCGCC 1658
 QY 3009 TCCCATCCCGGCTGCGCTCAAGCTGGAGAACCCGCTGAGCTACGCGGCTGGGC 3068
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 QY 3069 GCGTCGGCGGCGAGTCCGCTATGGGACCTGCGAGCCCTGCTATGCGGCGGTGAGC 3128
 Db 1719 GCGTCGGCGGCGAGTCCGCTATGGGACCTGCGAGCCCTGCTATGCGGCGGTGAGC 1778
 QY 3129 GGGACCCGCTTCTGGGTCAACCTCAGCCGCGCTTCTCTATCCCTGGCACACTCTCTTAC 3188
 Db 1779 GGGACCCGCTTCTGGGTCAACCTCAGCCGCGCTTCTCTATCCCTGGCACACTCTCTTAC 1838
 QY 3189 AGCCGAAGAGCCAGTTGTATGACCGCTGTGGTGGTGGGCTGGT-----GG 3239
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 QY 3240 GCGG 3299
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 QY 3840 AACCCAGAGCTGACGTGTACACATTTGAAGCTATGAATGACGCCATCTTTCTGAA 3899
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 QY 3900 TGTCTGGAAGCCATTGAGCAGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3959
 Db 2559 TGTCTGGAAGCCATTGAGCAGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2618
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 QY 4200 GCACAAGTCCCGGATGTACAGCCAGTGTCTCGAATGAGGACCTCTCTCAAGAGTTGG 4259
 Db 2859 GGCRAAGTCCCGGATGTACAGCCAGTGTCTCGAATGAGGACCTCTCTCAAGAGTTGG 2918
 QY 4260 ATGGCTCAAAATCACCCCGGAGGATTCCTGTCATGAAAGACACTGCTTCTTACAGCAT 4319
 Db 2919 ATGGCTCAAAATCACCCCGGAGGATTCCTGTCATGAAAGACACTGCTTCTTACAGCAT 2978
 QY 4320 TATTCAGTGGATGGCTGAAATCAAAATCTTTGATGAACTTCTGATGAATGAATACAT 4379
 Db 2979 TATTCAGTGGATGGCTGAAATCAAAATCTTTGATGAACTTCTGATGAATGAATACAT 3038
 QY 4380 CAAGGAACCTGATCGTATCATTTGATGAAAGGAAATCCACATCTCTGCTCAAGAG 4439
 Db 3039 CAAGGAACCTGATCGTATCATTTGATGAAAGGAAATCCACATCTCTGCTCAAGAG 3098
 QY 4440 CTTCTACAGCTCACCAAGCTCTGAGTCCGCTGAGCCTATTGGAGAGAGCTGCATCA 4499
 Db 3099 CTTCTACAGCTCACCAAGCTCTGAGTCCGCTGAGCCTATTGGAGAGAGCTGCATCA 3158
 QY 4500 GTTCACTTTTGAAGCTGATCAATCAAGTCAACATGTTGAGCTGGAGCTTTCGGAATGAT 4559
 Db 3159 GTTCACTTTTGAAGCTGATCAATCAAGTCAACATGTTGAGCTGGAGCTTTCGGAATGAT 3218
 QY 4560 GGCAGAGATCATCTCTGTCGAAGTCCGCTGAGTCCCTTCTGGAAAGTCAAGCTCATCA 4619
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 QY 4920 AATCTGTGATGATCTCTATATGCGGAGTGTCAAGTGTGCTGTTTGAATGCTGCTTGA 4979
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Db	1789	CTGTAGCCCCCTACGCTACACTCGGCCCCCTCAGGGCTCGCGGCCAGGAAGCGACT	1848
QY	3362	TCACCGCACCTGATGTGTGGTACCTTGGCGCATGGTGACGAGTGCCTATATCCCACTG	3421
Db	1849	TCACCGCACCTGATGTGTGGTACCTTGGCGCATGGTGACGAGTGCCTATATCCCACTG	1908
QY	3422	CCACTTGTGTCAAAAGCGAAATGGCCCTCGATGGATAGTACTATTAATTTCCACCCC	3481
Db	1909	CCACTTGTGTCAAAAGCGAAATGGCCCTCGATGGATAGTACTATTAATTTCCACCCC	1968
QY	3482	ACATSCGTTTGGAGACTGCCAGGACCATGTTTGGCCATTGACTATTAATTTCCACCCC	3541
Db	1969	ACATSCGTTTGGAGACTGCCAGGACCATGTTTGGCCATTGACTATTAATTTCCACCCC	2028
QY	3542	AGAAAGCTGCCTGATCTGTGGAGTGAAGCTTCTGGGTGTCACTATGAGCTCTCACAT	3601
Db	2029	AGAAAGCTGCCTGATCTGTGGAGTGAAGCTTCTGGGTGTCACTATGAGCTCTCACAT	2088
QY	3602	GTGGAAGCTGCAAGGTTCTTCTCAAAAGAGCCCTGAAGGAAACAGAACTGCTGGG	3661
Db	2089	GTGGAAGCTGCAAGGTTCTTCTCAAAAGAGCCCTGAAGGAAACAGAACTGCTGGG	2148
QY	3662	CCAGCAAAATGATTGCACTATTGATAAATTCGGAAGGAAATGTCTCATCTTGTGCTC	3721
Db	2149	CCAGCAAAATGATTGCACTATTGATAAATTCGGAAGGAAATGTCTCATCTTGTGCTC	2208
QY	3722	TTGGAAATGTTATGAAGCAGGATGACTCTGGAGCCCGGAAGCTGAAGAACTTGTA	3781
Db	2209	TTGGAAATGTTATGAAGCAGGATGACTCTGGAGCCCGGAAGCTGAAGAACTTGTA	2268
QY	3782	ATCTGAACTACAGGAGGAGAGGCTTCCAGCACCCAGCCCACTGAGGAGACAA	3841
Db	2269	ATCTGAACTACAGGAGGAGAGGCTTCCAGCACCCAGCCCACTGAGGAGACAA	2328
QY	3842	CCAGAACTGACAGTGCACACATTGAAGGCTATGAATGTGAGCCCATCTTCTGAATG	3901
Db	2329	CCAGAACTGACAGTGCACACATTGAAGGCTATGAATGTGAGCCCATCTTCTGAATG	2388
QY	3902	TCTTGAAGCCATTGAGCCAGGTGATGTGTGCTGGACAGACACAAACAGCCGACT	3961
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QY	3962	CCCTTGCAGCCTTGCTCTACGCTCAATGAACCTGGGAGAGACAGCTTGACACGTG	4021
Db	2449	CCCTTGCAGCCTTGCTCTACGCTCAATGAACCTGGGAGAGACAGCTTGACACGTG	2508
QY	4022	TCAAGTGGCCAAAGCCCTTGCTGCTTCCGCAACTTACAGTGGACACAGATGCTG	4081
Db	2509	TCAAGTGGCCAAAGCCCTTGCTGCTTCCGCAACTTACAGTGGACACAGATGCTG	2568
QY	4082	TCATTCAGTACTCCTGGATGGGCTCATGGTGTGGCATGGCTGGCATCTCTCACCA	4141
Db	2569	TCATTCAGTACTCCTGGATGGGCTCATGGTGTGGCATGGCTGGCATCTCTCACCA	2628
QY	4142	ATGTCAACTCCAGGATGCTTACTTCCGCTGATCTGGTTCATGAGTACCGATGC	4201
Db	2629	ATGTCAACTCCAGGATGCTTACTTCCGCTGATCTGGTTCATGAGTACCGATGC	2688
QY	4202	ACAACTCCCGATGACAGCAGTGTGCGAATGAGGCACCTCTCTCAAGAGTTTGGAT	4261
Db	2689	ACAACTCCCGATGACAGCAGTGTGCGAATGAGGCACCTCTCTCAAGAGTTTGGAT	2748
QY	4262	GGCTCCAAATCACCCCCAGGAATTCCTGTGTCATGAAGCACTGCTCTCTTCAGATTA	4321
Db	2749	GGCTCCAAATCACCCCCAGGAATTCCTGTGTCATGAAGCACTGCTCTCTTCAGATTA	2808
QY	4322	TTCCAGTGGATGGGCTGAAAAATCAAAAAATCTTTGATGAATTCGAATGAACATCA	4381
Db	2809	TTCCAGTGGATGGGCTGAAAAATCAAAAAATCTTTGATGAATTCGAATGAACATCA	2868
QY	4382	AGGAACTCGATCGTATCATTTGCATGCAAGGAAAAAATCCACATCTCTGCTCAAGACCT	4441

Db	2869	AGGAACTGATCGTATCATTTGTCATCAAAAGAAAAATCCACATCTCTGCTCAAGACGT	2928
QY	4442	TCATACAGCTCACCAGGCTCCTGGACTCCGTGCAGCCCTATTGCGAGAGAGTGCATCAGT	4501
Db	2929	TCATACAGCTCACCAGGCTCCTGGACTCCGTGCAGCCCTATTGCGAGAGAGTGCATCAGT	2988
QY	4502	TCACHTTTGACCTGCTAATCAAGTCACACATGGTGGAGCTTTCCGGAAATGATGG	4561
Db	2989	TCACHTTTGACCTGCTAATCAAGTCACACATGGTGGAGCTTTCCGGAAATGATGG	3048
QY	4562	CAGAGATCATCTCTGTCAGCTGCCCAAGATCCCTTTCTGGGAAAGTCAAGCCCTATT	4621
Db	3049	CAGAGATCATCTCTGTCAGCTGCCCAAGATCCCTTTCTGGGAAAGTCAAGCCCTATT	3108
QY	4622	TCCACACCCAGTGAAGCATTTGGAACCCCTATTTCCTCCACCCAGCTCATGCCCTTTCA	4681
Db	3109	TCCACACCCAGTGAAGCATTTGGAACCCCTATTTCCTCCACCCAGCTCATGCCCTTTCA	3168
QY	4682	GATGCTCTTCGCCCTGTTTATAACTCTGCACCTACTCCTCTGCAGTGCCTTGGGGAATTCCT	4741
Db	3169	GATGCTCTTCGCCCTGTTTATAACTCTGCACCTACTCCTCTGCAGTGCCTTGGGGAATTCCT	3228
QY	4742	CTAFTGATGTACAGTCTGTGCATGAACATGTCCTGAATCTATTTCCTGGGCTTTT	4801
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QY	4802	TCCTTTCTCTCTCTTTCTTTTCTTCCTCCCTCTATCAACCTCCCATGGCACCTTC	4861
Db	3289	TCCTTTCTCTCTCTTTCTTTTCTTCCTCCCTCTATCAACCTCCCATGGCACCTTC	3348
QY	4862	AGACTTTGCTTCCCATTTGGCTCCCTATCTGTGTTTGAATGGTGTGTATGCCCTTAA	4921
Db	3349	AGACTTTGCTTCCCATTTGGCTCCCTATCTGTGTTTGAATGGTGTGTATGCCCTTAA	3408
QY	4922	TCGTGATGATCTCATATGGCCAGTGTCAAGTTGTGCTTTTACAGCACTACTCTGT	4981
Db	3409	TCGTGATGATCTCATATGGCCAGTGTCAAGTTGTGCTTTTACAGCACTACTCTGT	3468
QY	4982	GCAGCCACACAAAGCTTTTACTTATCTATGCGCCGGAAGTTTAGAGAGCTAAGATTAT	5041
Db	3469	GCAGCCACACAAAGCTTTTACTTATCTATGCGCCGGAAGTTTAGAGAGCTAAGATTAT	3528
QY	5042	CTGGGGAATCAAAACAAAAACAAAGCAACAAAAA	5082
Db	3529	CTGGGGAATCAAAACAAAAACAAAGCAACAAAAA	3569
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LOCUS	Human androgen receptor (AR) mRNA, complete cds. PRI 31-OCT-1988		
DEFINITION	M20132 J03180		
ACCESSION	M20132.1 GI:178627		
VERSION	1 (bases 1 to 3569)		
KEYWORDS	Human, androgen receptor.		
SOURCE	Human, epididymal cDNA to mRNA, clones ARHEL[1-3] and ARHEL1.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
AUTHORS	Lubahn, D.B., Joseph, D.R., Sar, M., Tan, J., Higgs, H.N., Larson, R.E., French, F.S. and Willson, E.M.		
TITLE	The human androgen receptor: complementary deoxyribonucleic acid cloning, sequence analysis and gene expression in prostate		
JOURNAL	Mol. Endocrinol. 2 (12), 1265-1275 (1988)		
MEDLINE	89112208		
PUBMED	3216866		
COMMENT	Draft entry and computer readable sequence [1] kindly submitted by E.M.Wilson, 18-AUG-1988.		
FEATURES	Location/Qualifiers		
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	/organism="Homo sapiens"		
	/db_xref="taxon:9606"		

[illegible]

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QY	4322		TTCCAGTGGATGGGCTGAAAATCAAAATTTCTTTGATGAAC TTCGAATGAAC TACATCA	4381
Db	2809		TTCCAGTGGATGGGCTGAAAATCMAAATTTCTTTGATGAAC TTCGAATGAAC TACATCA	2868
QY	4382		AGGAAC TCGATCGTATCATTCGATGCAAAAGAAAAATCCACATCTCTGCTCAAGACGCT	4441
Db	2869		AGGAAC TCGATCGTATCATTCGATGCAAAAGAAAAATCCACATCTCTGCTCAAGACGCT	2928
QY	4442		TCTACCACTCACAAGCTCTCGAC TCCGTCGAGCCTATTGGAGAGAGCTGCATCAGT	4501
Db	2929		TCTACCACTCACAAGCTCTCGAC TCCGTCGAGCCTATTGGAGAGAGCTGCATCAGT	2988
QY	4502		TCAC TTTGACCTGCTAATCAAGTCACACATGCTGACGCTGGACTTTCGCGAATCATGG	4561
Db	2989		TCAC TTTGACCTGCTAATCAAGTCACACATGCTGACGCTGGACTTTCGCGAATCATGG	3048
QY	4562		CAGAGATCATCTCTGTCGAAGTCCCAAGATCCTTTCTGGGAAAGTCAAGCCATCTATT	4621
Db	3049		CAGAGATCATCTCTGTCGAAGTCCCAAGATCCTTTCTGGGAAAGTCAAGCCATCTATT	3108
QY	4622		TCCACACCCAGTGAAGCATTTGAAACCCCTATTTCGCCACCCAGCTCATGCCCTTTCA	4681
Db	3109		TCCACACCCAGTGAAGCATTTGAAACCCCTATTTCGCCACCCAGCTCATGCCCTTTCA	3168
QY	4682		GATGCTCTTCGCTGTTATAACTCTGCATCTCTCTCGAGTGCCTTGGGGAATTTCT	4741
Db	3169		GATGCTCTTCGCTGTTATAACTCTGCATCTCTCTCGAGTGCCTTGGGGAATTTCT	3228
QY	4742		CTATTGATGTACAGTCTGTCATGAACATGTTCTGAAATCTATTTCGCTGGGCTTTTTTT	4801
Db	3229		CTATTGATGTACAGTCTGTCATGAACATGTTCTGAAATCTATTTCGCTGGGCTTTTTTT	3288
QY	4802		TCCTTTCTCTCCTTTCTTTCTTCTCCCTCCTATCTAACCCTCCCATGGCACCTTC	4861
Db	3289		TCCTTTCTCTCCTTTCTTTCTTCTCCCTCCTATCTAACCCTCCCATGGCACCTTC	3348
QY	4862		AGACTTTGCTTCCCATTTGCTGGCTCCTATCTGTGTTTTCGAATGGTGTGTATGCCCTTAAA	4921
Db	3349		AGACTTTGCTTCCCATTTGCTGGCTCCTATCTGTGTTTTCGAATGGTGTGTATGCCCTTAAA	3408
QY	4922		TCGTGTATGATCCTCATATGGCCCAAGTGTCAAGTTGCTTGTATTACAGCACTACTCTGT	4981
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QY	4982		GCCAGCCACACAAAGTTTACTTATCTTATGCCACGGAGTTTATAGAGACTATGATTAT	5041
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RESULT 8	
HSDJ80804	
LOCUS	
DEFINITION	
ACCESSION	
VERSION	
KEYWORDS	
SOURCE	
ORGANISM	
REFERENCE	
AUTHORS	
TITLE	
JOURNAL	

HSDJ08004
 Human DNA sequence from clone R4-808O4 on chromosome Xq11.1-12,
 complete sequence.
 AL049564
 AL049564.11 GI:19338177
 HTG.
 human.
 homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 139033)
 Chapman, J.
 Direct Submission
 Submitted (08-MAR-2002) Wellcome Trust Sanger Institute, Hinxton,
 Cambridgeshire, CB10 1SA, UK. E-mail enquiries:

Db	103708	CCGAAATAAAGAAAAGATAATAACTCAGTTCCTTATTTGACCACTACTTCAGTGGACACT	103767
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Db	103828	ACCCTTCAAGTATTAAAGACAGACTGTGAGCTAGCAGGGCAGATCTTCTCCACCGTGT	103887
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Db	104008	CACAGCGCTGTGAACCTCTCTGACACAGAAAGGGAGCGGGTAAAGGAAGTAGGTGG	104067
QY	1843	AAGATTCAGCCAAAGCTCAAGGATGGAAGTGCAGTTAGGGCTGGGAAGGTCTACCTCGG	1902
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QY	1903	CGCGCGTCCAAGACCTACCGAGAGCTTCCAGAACTCTGTTCCAGAGCGTGGCGAAGTG	1962
Db	104128	CGCGCGTCCAAGACCTACCGAGAGCTTCCAGAACTCTGTTCCAGAGCGTGGCGAAGTG	104187
QY	1963	ATCCAGAACCCGGGCCCGAGCACCCAGAGCGCGAGCGAGCAGCACTCCCGGGCCCACT	2022
Db	104188	ATCCAGAACCCGGGCCCGAGCACCCAGAGCGCGAGCGAGCAGCACTCCCGGGCCCACT	104247
QY	2023	TTGCTGCTGCTGTCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG	2082
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Db	104362	GGTGAGGATGGTCTCCCAAGCCCATCGTAGAGGCCCAAGGCTACCTGGTCTCGAT	104421
QY	2203	GAGGAACAGCAACCTTCACAGCCGCACTGGCGCCCTGGAGTGCACCCGAGAGAGTTGC	2262
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QY	2323	CCTCCGACAGGATGACTCAGTGCCCATCCAGTTGCTCCCTGCTGGGCCCATCTTC	2382
Db	104542	CCTCCGACAGGATGACTCAGTGCCCATCCAGTTGCTCCCTGCTGGGCCCATCTTC	104601
QY	2383	CCGGCTTAAGCAGCTGCTCCGTGACCTTAAAGACATCTCTGAGCGAGGCCAGCACCATG	2442
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QY	2443	CAACTCTCTCAGCAACAGCAGCAGCAAGCAGTATCCGAGCGCAGCAGCGGGAGCGG	2502
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QY	2503	AGGGAGGCTCGGGGCTCCCACTTCTCTCCAAAGACAAATTAATTAGGGGCACTTCGACC	2562
Db	104722	AGGGAGGCTCGGGGCTCCCACTTCTCTCCAAAGACAAATTAATTAGGGGCACTTCGACC	104781
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Db 104782 ATTTCTGACAAACGCCAAGGAGTTGTGTAAGGCAGTGTCSGTCTCCATGGGCGCTTGGTGTG 104841

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QY 2803 TTCAAGGGAGTTTACACCAAGGGCTAGAAGCGAGAGCCCTAGGCTCTCTGCGACGCT 2862

Db 105022 TTCAAGGGAGTTTACACCAAGGGCTAGAAGCGAGAGCCCTAGGCTCTCTGCGACGCT 105081

QY 2863 GCAGCAGGAGCTCCGGGACACTTGAATCGGCTTACCTGTCTACCTGTCTCTACAAAGTCCGGA 2922

Db 105082 GCAGCAGGAGCTCCGGGACACTTGAATCGGCTTACCTGTCTCTACAAAGTCCGGA 105141

QY 2923 GCATGGACAGGCACTCGCTACAGAGTGCAGACTTACAACTTTCCACTGGGCTGTG 2982

Db 105142 GCATGGACAGGCACTCGCTACAGAGTGCAGACTTACAACTTTCCACTGGGCTGTG 105201

QY 2983 GCGGACAGCGCGCCCTCCGCGGCTCCCATCCCGACGCTCGCATCCAGGTGAGAAC 3042

Db 105202 GCGGACAGCGCGCCCTCCGCGGCTCCCATCCCGACGCTCGCATCCAGGTGAGAAC 105261

QY 3043 CCGCTGGACTACGGCAGCGCTTGGGCGGCTCGCGCGGCGCAGTGCCTATGGGACCTG 3102

Db 105262 CCGCTGGACTACGGCAGCGCTTGGGCGGCTCGCGCGGCGCAGTGCCTATGGGACCTG 105321

QY 3103 GCGACCTTCATGCGGGGTGACGGGACCGCGTTCTTGGGTCACTTCAGCCGCCCT 3162

Db 105322 GCGACCTTCATGCGGGGTGACGGGACCGCGTTCTTGGGTCACTTCAGCCGCCCT 105381

QY 3163 TCCTCATCCTGGCACACTCTTTCACAGCGCAAGAGGCCAGTTGTATGGACCGTGTGT 3222

Db 105382 TCCTCATCCTGGCACACTCTTTCACAGCGCAAGAGGCCAGTTGTATGGACCGTGTGT 105441

QY 3223 GGTGTGGGGTGTGCGCGCGGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 3282

Db 105442 GGTGTGGGGTGTG---GCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 105498

QY 3283 GCGCGCGCGAGCGGAGTGTAGCCCTCTACGGCTACACTTCGGCCCTCTCAGGGGCTG 3342

Db 105499 GCGCGCGCGAGCGGAGTGTAGCCCTCTACGGCTACACTTCGGCCCTCTCAGGGGCTG 105558

QY 3343 GCGGGCCAGAAAGCACTTCACCGACCTGATGTGGTACCTTGGCGCATGTGTGAGC 3402

Db 105559 GCGGGCCAGAAAGCACTTCACCGACCTGATGTGGTACCTTGGCGCATGTGTGAGC 105618

QY 3403 AGATGCCCTATCCCACTCCCACTTGTGTCAAAAGCAAAATGGCCCTGTATGATAGC 3462

Db 105619 AGATGCCCTATCCCACTCCCACTTGTGTCAAAAGCAAAATGGCCCTGTATGATAGC 105678

QY 3463 TACTTCGGACCTTACGGGACATGGCTT 3490

Db 105679 TACTTCGGACCTTACGGGACATGGCTT 105706

RESULT 9	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM
	HUMARX	3231 bp mRNA linear	PRI 31-OCT-1994				
		Human androgen-receptor mRNA; complete cds.					
	M34233						
	M34233.1	GI:179033					
		androgen receptor.					
		Human testis and prostate cancer cell line LNCaP, cdna to mRNA.					
		Homo sapiens					
		Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;					

[illegible]

Db	1456	-----GGCGGGCGCGCGCGCGCGCGCGCGAGCGGGAGCTGTAGCCCCCTAC	1509
QY	3316	GGCTACACTGCGCCCCCTCAGGGGCTGGCGGGCCAGGAAGCGACTTCACCGCACCTGAT	3375
Db	1510	GGCTACACTGCGCCCCCTCAGGGGCTGGCGGGCCAGGAAGCGACTTCACCGCACCTGAT	1569
QY	3376	GTGTGGTACCCCTGGCGCATGGTGAGCAGAGTGCCTATATCCAGTCCACATGTGTGTCAAA	3435
Db	1570	GTGTGGTACCCCTGGCGCATGGTGAGCAGAGTGCCTATATCCAGTCCACATGTGTGTCAAA	1629
QY	3436	ACGGAATAGGCGCCCTGGATGGATAGCTACTCGGACCTTACGGGACATGCCTTTGGAG	3495
Db	1630	ACGGAATAGGCGCCCTGGATGGATAGCTACTCGGACCTTACGGGACATGCCTTTGGAG	1689
QY	3496	ACTGCCAGGGACCATGTTTGGCCATTGACTATATCTTCCACCCACAGACCTGCCTG	3555
Db	1690	ACTGCCAGGGACCATGTTTGGCCATTGACTATATCTTCCACCCACAGACCTGCCTG	1749
QY	3556	ATCTCTGGAGATGAAGCTTCTGGGTGTCACTATGAGAGCTTCACATGTGAAAGCTGCAAG	3615
Db	1750	ATCTCTGGAGATGAAGCTTCTGGGTGTCACTATGAGAGCTTCACATGTGAAAGCTGCAAG	1809
QY	3616	GTCTTCTTCAAAGAGCGCTGAAGGAAACAGAAAGTACCTGTCGGCCACACAGAAATGAT	3675
Db	1810	GTCTTCTTCAAAGAGCGCTGAAGGAAACAGAAAGTACCTGTCGGCCACACAGAAATGAT	1869
QY	3676	TGCACTATTGATAAATTCGAGGAAAATGTCCATCTTGCTCTTCGGAATGTTAT	3735
Db	1870	TGCACTATTGATAAATTCGAGGAAAATGTCCATCTTGCTCTTCGGAATGTTAT	1929
QY	3736	GAAGCAGGGATGACTCTGGAGCGCCGGAAGCTGAGAAACTTGGTATCTGAACTACAG	3795
Db	1930	GAAGCAGGGATGACTCTGGAGCGCCGGAAGCTGAGAAACTTGGTATCTGAACTACAG	1989
QY	3796	GAGGAGGAGAGGCTTCCAGCACACCAGCCCACTGAGGAGACAACCCAGAGCTGACA	3855
Db	1990	GAGGAGGAGAGGCTTCCAGCACACCAGCCCACTGAGGAGACAACCCAGAGCTGACA	2049
QY	3856	GTGTCAACACTGAAGGCTATGAATGTGAGCCCATCTTCTGAAATGCTCTGGAAGCCATT	3915
Db	2050	GTGTCAACACTGAAGGCTATGAATGTGAGCCCATCTTCTGAAATGCTCTGGAAGCCATT	2109
QY	3916	GAGCAGGTGTAGTGTGTCTGGACACACAAACAGCCGACCTTTCAGAGCTTG	3975
Db	2110	GAGCAGGTGTAGTGTGTCTGGACACACAAACAGCCGACCTTTCAGAGCTTG	2169
QY	3976	CTCTCTAGCCTCAATGAACCTGGGAGAGACAGCTTGTACAGTGGTCAAGTGGGCCAAG	4035
Db	2170	CTCTCTAGCCTCAATGAACCTGGGAGAGACAGCTTGTACAGTGGTCAAGTGGGCCAAG	2229
QY	4036	GCCTTCCCTGGCTCCGCAACTTACAGTGGAGACACAGTGGTGTCAAGTGGTCAAGTGGGCCAAG	4095
Db	2230	GCCTTCCCTGGCTCCGCAACTTACAGTGGAGACACAGTGGTGTCAAGTGGTCAAGTGGGCCAAG	2289
QY	4096	TGATGGGCTCATGGTGTTCGATGGGTGGCGATCTTCCAAATGTCAACTCCAGG	4155
Db	2290	TGATGGGCTCATGGTGTTCGATGGGTGGCGATCTTCCAAATGTCAACTCCAGG	2349
QY	4156	ATGCTCTACTTGGCCCTGATCTGGTTTCAATGAGTACCGCATGCACAAGTCCCGGATG	4215
Db	2350	ATGCTCTACTTGGCCCTGATCTGGTTTCAATGAGTACCGCATGCACAAGTCCCGGATG	2409
QY	4216	TACAGCAGTGTGTCCGAATGAGGCACCTCTCTCAGAGTGTGGATGGCTCCAAATCAC	4275
Db	2410	TACAGCAGTGTGTCCGAATGAGGCACCTCTCTCAGAGTGTGGATGGCTCCAAATCAC	2469
QY	4276	CCCCAGGAATTCCTGTGCATCAAGCAGCTGCTACTCTTCAGATTATTCAGTGGATGG	4335
Db	2470	CCCCAGGAATTCCTGTGCATCAAGCAGCTGCTACTCTTCAGATTATTCAGTGGATGG	2529
QY	4336	CTGAAAAATCAAAAATCTTTGATGAACHTTCGAATGAACATCAAGGAACCTCGATCT	4395

Db	2530	CTGAAAAATCAAAAATCTTTTGATGAACCTTCCAATGAACATACATCAAGGAACCTGATCGT	2589
Qy	4396	ATCATTTGCATCAAAAGAAAAATCCCAATCCTGCTCAAGACGCTTCTACCAAGCTCAAC	4455
Db	2590	ATCATTTGCATCAAAAGAAAAATCCCAATCCTGCTCAAGACGCTTCTACCAAGCTCAAC	2649
Qy	4456	AAGCTCTCGGACTCCGTTGACGCTATTTCGAGAGAGCTGCATCAGTTTCACCTTTTGACCTG	4515
Db	2650	AAGCTCTCGGACTCCGTTGACGCTATTTCGAGAGAGCTGCATCAGTTTCACCTTTTGACCTG	2709
Qy	4516	CTAATCAAGTCACACATGTTGAGCTTCCCGAAATGATGGCAGAGATCATCTCT	4575
Db	2710	CTAATCAAGTCACACATGTTGAGCTTCCCGAAATGATGGCAGAGATCATCTCT	2769
Qy	4576	GTGCAAGTGCCCAAGATCTTTTCGGAAGTCAAGCCCATCTATTTCACACCCAGTGA	4635
Db	2770	GTGCAAGTGCCCAAGATCTTTTCGGAAGTCAAGCCCATCTATTTCACACCCAGTGA	2829
Qy	4636	AGCATTGGAACCCCTATTTCGCCACCCAGCTCATGCCCTTTTCAGATGCTTTCGCTCT	4695
Db	2830	AGCATTGGAACCCCTATTTCGCCACCCAGCTCATGCCCTTTTCAGATGCTTTCGCTCT	2889
Qy	4696	GTTATAACTCTGCATCTCTCTGCAGTGCCTTGGGGAATTTCCCTCTATTGAATACAG	4755
Db	2890	GTTATAACTCTGCATCTCTCTGCAGTGCCTTGGGGAATTTCCCTCTATTGAATACAG	2949
Qy	4756	TCCTGTCATGAACATGTTCTGTAATCTATTTCGCTGGGCTTTTTCCTCTCTCTCTCT	4815
Db	2950	TCCTGTCATGAACATGTTCTGTAATCTATTTCGCTGGGCTTTTTCCTCTCTCTCTCT	3009
Qy	4816	TTCTTTTCT	4875
Db	3010	TTCTTTTCT	3069
Qy	4876	ATTGTGGCT	4935
Db	3070	ATTGTGGCT	3128
Qy	4936	CATATGGCCCAAGTGTCAAGTTGTCTTGTATACACACTACTCTCTGCGCCACACACAAA	4995
Db	3129	CATATGGCCCAAGTGTCAAGTTGTCTTGTATACACACTACTCTCTGCGCCACACACAAA	3187
Qy	4996	CGTTTACTTACTTATATGCGCGGGAATTT	5024
Db	3188	CGTTTACTTACTTATGCGCGGGAATTT	3216
RESULT 10			
HUMANRE			
LOCUS			
DEFINITION			
ACCESSION			
VERSION			
KEYWORDS			
SOURCE			
ORGANISM			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
MEDLINE			
PUBMED			
FEATURES			
source			
gene			

Db	1708	ATCTGTGGAGATGAAGCTTCTGGGTGTCACTATGAGGCTCTCACATGTGGAGCTGCAAG	1767
QY	3616	GTCTTCTTCAAAAGAGCGCTGAAGGGAAACAGAAAGTACCTGTGCGCCAGCAGAAATGAT	3675
Db	1768	GTCTTCTTCAAAAGAGCGCTGAAGGGAAACAGAAAGTACCTGTGCGCCAGCAGAAATGAT	1827
QY	3676	TGCACATTTGATAATTCGGAAGGAAAATTTGCCATCTTGTCTCTTCGGAATGTTAT	3735
Db	1828	TGCACATTTGATAATTCGGAAGGAAAATTTGCCATCTTGTCTCTTCGGAATGTTAT	1887
QY	3736	GAAGCAGGAGTACTCTGTGGAGCCCGAAGCTGAAGAAACTTGGTAACTTGAACATACAG	3795
Db	1888	GAAGCAGGAGTACTCTGTGGAGCCCGAAGCTGAAGAAACTTGGTAACTTGAACATACAG	1947
QY	3796	GAGGAAGAGAGGCTTCCAGCACACAGACGCCCACTGAGGAGACAACCCAGAAGCTGACA	3855
Db	1948	GAGGAAGAGAGGCTTCCAGCACACAGACGCCCACTGAGGAGACAACCCAGAAGCTGACA	2007
QY	3856	GTGTACACATTTGAAGCTATGATGTACGCCCATCTTTCTGAATGTCTTGAAGCCATT	3915
Db	2008	GTGTACACATTTGAAGCTATGATGTACGCCCATCTTTCTGAATGTCTTGAAGCCATT	2067
QY	3916	GAGCCAGGTGTAGTGTGTGTGGACAGCAACAACCCAGCCGAGCTCTTTGCAGCCTTG	3975
Db	2068	GAGCCAGGTGTAGTGTGTGTGGACAGCAACAACCCAGCCGAGCTCTTTGCAGCCTTG	2127
QY	3976	CTCTCTAGCCTCAATGAAGCTGGAGAGACAGACCTTGTACAGTGGTCAAGTGGGCCAAG	4035
Db	2128	CTCTCTAGCCTCAATGAAGCTGGAGAGACAGACCTTGTACAGTGGTCAAGTGGGCCAAG	2187
QY	4036	GCCTTGCCCTTCGCGCAACTTTACAGCTGGAGCAGCAGATGGCTGTCTCATTCAGTACTCC	4095
Db	2188	GCCTTGCCCTTCGCGCAACTTTACAGCTGGAGCAGCAGATGGCTGTCTCATTCAGTACTCC	2247
QY	4096	TGATGGGCTCATGTGTTTGGCCATGGCTGGGATCCTTCCACAAATGTCAACTTCCAGG	4155
Db	2248	TGATGGGCTCATGTGTTTGGCCATGGCTGGGATCCTTCCACAAATGTCAACTTCCAGG	2307
QY	4156	ATGCTCTACTTCGCCCCGTGATCTGGTTTTCAATGATAGTACCGCATGCACAACTCCGATG	4215
Db	2308	ATGCTCTACTTCGCCCCGTGATCTGGTTTTCAATGATAGTACCGCATGCACAACTCCGATG	2367
QY	4216	TACAGCCAGTGTGTCGGATGAGGCACCTCTCTCAAGAGTTGGATGGCTCCAATCACC	4275
Db	2368	TACAGCCAGTGTGTCGGATGAGGCACCTCTCTCAAGAGTTGGATGGCTCCAATCACC	2427
QY	4276	CCCCAGGAATCCTGTGCATGAAGACACTGTGA-----CTCTTC	4314
Db	2428	CCCCAGGAATCCTGTGCATGAAGACCACTGCTAATTTTTTTTTTTTGGTCTCTCTTC	2487
QY	4315	AGCATTTATCCAGTGGATGGCTGAAATCAAAAATCTTTTGTATGAACCTCGAATGAAC	4374
Db	2488	AGCATTTATCCAGTGGATGGCTGAAATCAAAAATCTTTTGTATGAACCTCGAATGAAC	2547
QY	4375	TACATCAAGGAACTCGATCGTATCATTTGCATGCAAAAAGAAAAATCCACATCTCGTCA	4434
Db	2548	TACATCAAGGAACTCGATCGTATCATTTGCATGCAAAAAGAAAAATCCACATCTCGTCA	2607
QY	4435	AGACGCTTCTACCAAGCTCACCAAGCTCCTGGACTCCTGGAGCCTATTCGAGAGAGCTG	4494
Db	2608	AGACGCTTCTACCAAGCTCACCAAGCTCCTGGACTCCTGGAGCCTATTCGAGAGAGCTG	2667
QY	4495	CATCAGTTTCACTTTTGGACTCTAATCAAGTTCACACATGTGAGCGTGGACTTTCCGGAA	4554
Db	2668	CATCAGTTTCACTTTTGGACTCTAATCAAGTTCACACATGTGAGCGTGGACTTTCCGGAA	2727
QY	4555	ATGATGCGAGAGATCATCTGTGCAAGTGCCTAAGTATCTTCTGGGAAAGTCAAGCCC	4614
Db	2728	ATGATGCGAGAGATCATCTGTGCAAGTGCCTAAGTATCTTCTGGGAAAGTCAAGCCC	2787
QY	4615	ATCTATTTCACACCCAGTGAAGCATTTGGAAACCCCTATTTTCCCCACCCAGCTATGCC	4674
Db	2788	ATCTATTTCACACCCAGTGAAGCATTTGGAAACCCCTATTTTCCCCACCCAGCTATGCC	2847

[illegible]

QY	2944	TACAGAGTCCGAC	TACTACAACTTCCACTGGCTCTGGCGGACCGCGCCCTCCG	3000
DB	1066	TACAGAGTCCGAC	TACTACAACTTCCACTGGCTCTGGCGGACCGCGCCCTCCG	1125
QY	3004	CCGCTCCCAT	CCCCACGCTCGCATCAAGCTGGAGAACCCGCTGGACTACGGCAGCGCC	3063
DB	1126	CCGCTCCCAT	CCCCACGCTCGCATCAAGCTGGAGAACCCGCTGGACTACGGCAGCGCC	1185
QY	3064	TGGCGGCT	CGGCGGCGAGTCCCGCTATGGGGACCTGGCGAGCCTGCATGGCGGGT	3123
DB	1186	TGGCGGCT	CGGCGGCGAGTCCCGCTATGGGGACCTGGCGAGCCTGCATGGCGGGT	1245
QY	3124	GCAGGGAC	CCGGTCTGGGTCAACCTCAGCGCGCGTTCCTCATCTCGCACACTTC	3183
DB	1246	GCAGGGAC	CCGGTCTGGGTCAACCTCAGCGCGCGTTCCTCATCTCGCACACTTC	1305
QY	3184	TTCCAGCCG	GAAGGCCAGTTGTATGAGACGCTGTGTGGTGTGGGTGGTGGCGC	3243
DB	1306	TTCCAGCCG	GAAGGCCAGTTGTATGAGACGCTGTGTGGTGTGGGTGGTGGCGC	1359
QY	3244	GCGCGCGC	GGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGAGT	3303
DB	1360	-----	GGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGAGT	1404
QY	3304	GTAGCCCT	TACGCTTACACTCGGCCCTTCAGGGCTGGCGGCGAGAAAGCACTTC	3363
DB	1405	GTAGCCCT	TACGCTTACACTCGGCCCTTCAGGGCTGGCGGCGAGAAAGCACTTC	1464
QY	3364	ACCGACCT	GATGTGTGTACCTGGCGCATGCTCAGCAGAGTGCCTATCCCAAGTCC	3423
DB	1465	ACCGACCT	GATGTGTGTACCTGGCGCATGCTCAGCAGAGTGCCTATCCCAAGTCC	1524
QY	3424	ACTTGT	CAAAAGCAATGGGCCCTGGATGGATGCTACTCCGGACCTTACGGGAC	3483
DB	1525	ACTTGT	CAAAAGCAATGGGCCCTGGATGGATGCTACTCCGGACCTTACGGGAC	1584
QY	3484	ATCGCT	TGGAGACTGCCAGGACCATGTTTGGCCATTGACTATTACTTTCCACCCAG	3543
DB	1585	ATCGCT	TGGAGACTGCCAGGACCATGTTTGGCCATTGACTATTACTTTCCACCCAG	1644
QY	3544	AGACCT	CGCTGATCTGTGGAGATGAAGCTTCTGGGTGTCACTATGGAGCTCTCACTGT	3603
DB	1645	AGACCT	CGCTGATCTGTGGAGATGAAGCTTCTGGGTGTCACTATGGAGCTCTCACTGT	1704
QY	3604	GGAAGT	CGAAGTCTTCTTCAAAGAGCCGCTGAAGGAAACAGAACTACCTGGCGCC	3663
DB	1705	GGAAGT	CGAAGTCTTCTTCAAAGAGCCGCTGAAGGAAACAGAACTACCTGGCGCC	1766
QY	3664	AGCAGAA	TGATTCACATTTCCGAAGAAAAATGTCCATCTGTCTGTCT	3722
DB	1765	AGCAGAA	TGATTCACATTTCCGAAGAAAAATGTCCATCTGTCTGTCT	1822
QY	3724	CGGAAAT	TGTTATGAAGCAGGATGACTCTGGAGCCCGGAAGCTGAAGAACTTGGTAAT	3783
DB	1825	CGGAAAT	TGTTATGAAGCAGGATGACTCTGGAGCCCGGAAGCTGAAGAACTTGGTAAT	1883
QY	3784	CTGAACT	ACAGGAGGAGAGGAGCTTCCAGCACCCACAGCCCGCTGAGGAGACAAC	3843
DB	1885	CTGAACT	ACAGGAGGAGGAGAGGCTTCCAGCACCCACAGCCCGCTGAGGAGACAAC	1943
QY	3844	CAGAAGT	CACAGTGTACACATTGAAGGCTATGAATGTACGCCATCTTCTGATGTC	3903
DB	1945	CAGAAGT	CACAGTGTACACATTGAAGGCTATGAATGTACGCCATCTTCTGATGTC	2003
QY	3904	CTGGAAGC	CAATGAGTGTGTGTGACACAGCAACAACACCGCCGACTCC	3963
DB	2005	CTGGAAGC	CAATGAGTGTGTGTGACACAGCAACAACACCGCCGACTCC	2063
QY	3964	TTTCAGC	CTTGTCTTAGCCTCAATGAACCTGGGAGAGACAGCTTGTACAGTGGTC	4023
DB	2065	TTTCAGC	CTTGTCTTAGCCTCAATGAACCTGGGAGAGACAGCTTGTACAGTGGTC	2123
QY	4024	AAGTGG	CCCAAGGCTTGGCTTCCCAACTTACAGTGGAGCAGCAATGGCTGTC	4083

Db	2125		AAATGGGCGAAGCGCTTCCTGGCTTCGGCAACTTACACGTGGACGACGATGGCTGTC	2184
Qy	4084		ATTCACTACTCTCGATGGGCTCATGGTGTTCCTCCATGGCTGGCGATGCTTCACCAAT	4143
Db	2185		ATTCACTACTCTCGATGGGCTCATGGTGTTCCTCCATGGCTGGCGATGCTTCACCAAT	2244
Qy	4144		GTCACACTCCAGATGCTCTACTTCGCCCTCGATCTGGTTCATAGTACCGCATGCAC	4203
Db	2245		GTCACACTCCAGATGCTCTACTTCGCCCTCGATCTGGTTCATAGTACCGCATGCAC	2304
Qy	4204		AAATCCCGATGTACAGCCAGTGTCCGAATCAGCACCTCTCTCAAGAGTTTGGATGG	4263
Db	2305		AAATCCCGATGTACAGCCAGTGTCCGAATCAGCACCTCTCTCAAGAGTTTGGATGG	2364
Qy	4264		CTCCAAATCACCCCGCAGGAATCTCTGTCATGAAGCACTGCTACTCTTCAGCATATT	4323
Db	2365		CTCCAAATCACCCCGCAGGAATCTCTGTCATGAAGCACTGCTACTCTTCAGCATATT	2424
Qy	4324		CAATGGATGGGCTGAAAAATCAAAATCTTTGATGAACCTTCGAATGAATACATCAAG	4383
Db	2425		CAATGGATGGGCTGAAAAATCAAAATCTTTGATGAACCTTCGAATGAATACATCAAG	2484
Qy	4384		GAATTCGATCGTATCATTTGATGCAAGAAAAATCCACATCTCTGCTCAAGACGCTTC	4443
Db	2485		GAATTCGATCGTATCATTTGATGCAAGAAAAATCCACATCTCTGCTCAAGACGCTTC	2544
Qy	4444		TACAGCTCACCAAGTCTCTGGACTCCGTCAGAGCTTTCGAGAGAGCTGCATCAGTTC	4503
Db	2545		TACAGCTCACCAAGTCTCTGGACTCCGTCAGAGCTTTCGAGAGAGCTGCATCAGTTC	2604
Qy	4504		ACTTTTACCTGCTATCAAGTCACACATGGTGGAGCTGGACTTTCGGAAAAATGATGGCA	4563
Db	2605		ACTTTTACCTGCTATCAAGTCACACATGGTGGAGCTGGACTTTCGGAAAAATGATGGCA	2664
Qy	4564		GAGATCATCTCTGTCAAGTGCCCAAGATCCCTTTCTGGAAAGTCAAGCCATCTATTTC	4623
Db	2665		GAGATCATCTCTGTCAAGTGCCCAAGATCCCTTTCTGGAAAGTCAAGCCATCTATTTC	2724
Qy	4624		CACACCCAGTGAAGCATTTGAAA-CCCTATTTCGCCACCCAGCTCATGCCCTTTTCAG	4682
Db	2725		CACACCCAGTGAAGCATTTGAAAACCCCTATTTCGCCACCCAGCTCATGCCCTTTTCAG	2784
Qy	4683		ATGCTCTTCGCTGTATAAAGTCTGCATCTCTCTGAGTGGAGTGGGAAATTCCTTC	4742
Db	2785		ATGCTCTTCGCTGTATAAAGTCTGCATCTCTCTGAGTGGAGTGGGAAATTCCTTC	2844
Qy	4743		TATTGATGTACAGTCTGTCAATGAAC	4767
Db	2845		TATTGATGTACAGTCTGTCAATGAAC	2869
RESULT	13			
LOCUS	AF162704			
DEFINITION	Homo sapiens cell-line MDA-MB-453 androgen receptor mRNA, complete cds.	2827 bp	linear	PRI 29-JUL-1999
ACCESSION	AF162704			
VERSION	AF162704.1	GI:5639998		
KEYWORDS				
SOURCE	Homo sapiens			
ORGANISM	Homo sapiens			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
AUTHORS	1 (bases 1 to 2827)			
TITLE	Jin, C.H., Urcan-Bisel, M.S. and Schrader, W.T.			
JOURNAL	Androgen receptor sequences in human mammary carcinoma MDA-MB-453 cells			
REFERENCE	Unpublished			
AUTHORS	2 (bases 1 to 2827)			
TITLE	Jin, C.H., Urcan-Bisel, M.S. and Schrader, W.T.			
JOURNAL	Direct Submission			
	Submitted (25-JUN-1999) Endocrine Research, Ligand Pharmaceuticals			

[illegible]

Db	1570	GACATGCTTTGGAGACTGCCAGGACCATGTTTGGCCATTGACTATTATACCTTCCACC	1629
Qy	3541	CAGAAGACCTGCCTGATCTCTGTGAGATGAAGCTTCTGGGTGTCACATATGAGCTCTCACA	3600
Db	1630	CAGAAGACCTGCCTGATCTCTGTGAGATGAAGCTTCTGGGTGTCACATATGAGCTCTCACA	1689
Qy	3601	TGTGGAAGCTCAAGGTCTTCTTCAAAGAGCCGCTGAAGGGAACAGAAAGTACCTGTGC	3660
Db	1690	TGTGGAAGCTGCCAAGTCTTCTTCAAAGAGCCGCTGAAGGGAACAGAAAGTACCTGTGC	1749
Qy	3661	GCCAGCAGAAATGATTTGCACATTTATGATAAATTCGGAGGAAAAATTTGCATCTTCTGCT	3720
Db	1750	GCCAGCAGAAATGATTTGCACATTTATGATAAATTCGGAGGAAAAATTTGCATCTTCTGCT	1809
Qy	3721	CTTTCGGAATGTATTAAGCAGAGGATGACTCTGGAGCCCGGAGCTGAAGAAACCTTGGT	3780
Db	1810	CTTTCGGAATGTATTAAGCAGAGGATGACTCTGGAGCCCGGAGCTGAAGAAACCTTGGT	1869
Qy	3781	AATCTGAACTACAGGAGGAGAGGCTTCCAGCACACACCAGCCCCACTGAGGAGACA	3840
Db	1870	AATCTGAACTACAGGAGGAGAGGCTTCCAGCACACACCAGCCCCACTGAGGAGACA	1929
Qy	3841	ACCCAGAAGCTGACAGTGTACACATTTGAAGGCTATGAATGTAGCCCATCTTCTTGAAT	3900
Db	1930	ACCCAGAAGCTGACAGTGTACACATTTGAAGGCTATGAATGTAGCCCATCTTCTTGAAT	1989
Qy	3901	GTCTCTGGAAGCCATTGAGCCAGGTGACTGTGCTGGACACGACAACAACACGCCCGAC	3960
Db	1990	GTCTCTGGAAGCCATTGAGCCAGGTGACTGTGCTGGACACGACAACAACACGCCCGAC	2049
Qy	3961	TCCCTTTCAGACCTTGTCTCTTAGCCCTCAATGAATCTGGGAGAGACAGCTTGTACAGTG	4020
Db	2050	TCCCTTTCAGACCTTGTCTCTTAGCCCTCAATGAATCTGGGAGAGACAGCTTGTACAGTG	2109
Qy	4021	GTCAAGTGGCCNAGGCTTGCCTGCTTCCGCAACTTACAGCTGGAGCAGACAGATGGCT	4080
Db	2110	GTCAAGTGGCCNAGGCTTGCCTGCTTCCGCAACTTACAGCTGGAGCAGACAGATGGCT	2169
Qy	4081	GTCAATTCAGTACTCTCTGGATGGGGCTCATGGTGTGGCATGGGTGGGATCTTCACT	4140
Db	2170	GTCAATTCAGTACTCTCTGGATGGGGCTCATGGTGTGGCATGGGTGGGATCTTCACT	2229
Qy	4141	AATGTCAACTCCAGGATGCTTACTTCGCCCTTGATCTGGTGTTCATATGAGTACGCCATG	4200
Db	2230	AATGTCAACTCCAGGATGCTTACTTCGCCCTTGATCTGGTGTTCATATGAGTACGCCATG	2289
Qy	4201	CACAAGTCCCGGATGTACAGCCAGTGTGCCAATCAGGCACCTCTCTCAAGATTGGA	4260
Db	2290	CACAAGTCCCGGATGTACAGCCAGTGTGCCAATCAGGCACCTCTCTCAAGATTGGA	2349
Qy	4261	TGGCTCCAAATCACCCCCAGGAATTCCTGTGCATGAAAGCACTGCTACTCTTACGATTT	4320
Db	2350	TGGCTCCAAATCACCCCCAGGAATTCCTGTGCATGAAAGCACTGCTACTCTTACGATTT	2409
Qy	4321	ATTCAGTGGATGGGCTGAAAAATTCAAAAATTTCTTTGTAGCACTTCGAATGAACTACATC	4380
Db	2410	ATTCAGTGGATGGGCTGAAAAATTCAAAAATTTCTTTGTAGCACTTCGAATGAACTACATC	2469
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Db	2590	TTCACTTTTGACCTGCTTAATCAAGTCACACATGGTGAAGCTGGACTTTCCGGAAATGATG	2649
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Db 2710 TTCCACACCCAGTGAAGATGGAAACCCCTATTTCCACCCAGTCCATGCCCCCTTTC 2769
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RESULT 14
LOCUS MFU94179
DEFINITION Macaca fascicularis androgen receptor mRNA, complete cds.
ACCESSION U94179
VERSION U94179.1 GI:3861480
KEYWORDS
SOURCE Macaca fascicularis.
ORGANISM Macaca fascicularis.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
Cercopithecinæ; Macaca.
1 (bases 1 to 2821)
Choong,C.S., Kempainen,J.A. and Willson,E.M.
Evolution of the primate androgen receptor: a structural basis for
disease
J. Mol. Evol. 47 (3), 334-342 (1998)
98404153
7932460
2 (bases 1 to 2821)
Choong,C.S., Kempainen,J.A. and Willson,E.M.
Direct Submission
Submitted (18-MAR-1997) Laboratories for Reproductive Biology,
University of North Carolina at Chapel Hill, CB 7500, MSRB, Rm 370,
UNC-CH, Chapel Hill, NC 27599, USA
LOCATION/Qualifiers
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/db_xref="GI:3861481"
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BASE COUNT 623 a 829 c 799 g 570 t
ORIGIN

Query Match
Best Local Similarity 51.48; Score 2612.4; DB 9; Length 2821;
Matches 2771; Conservative 0; Mismatches 46; Indels 91; Gaps 4;

QY 1864. ATGGAGTGCAGTTAGGCTGGGAGGCTACTACCTCGCGCGCTCCAGACCTACCGA 1923
Db 1 ATGGAGGTGCAGTTAGGCTGGGAGGCTACTACCTCGCGCGCGCTCCAGACCTACCGA
QY 1924 GGAGCTTCCAGATCTGTTCCAGAGGTGGCGAGTGTATCCAGAACCCGCCCCAGG 1983
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 Db 1141 GCCTGGCGGCTCGCGCGCAGTCCGCTATGGGACCTGGGAGCCTGCATGGCGCG 1200
 QY 3121 GGTGCAGCGGACCCGGTCTGGGTCAACCTCAGCGCGCTTCTCATCTGCACACT 3180
 Db 1201 GGTGCAGCGGACCCGGTCTGGGTCAACCTCAGCGCGCTTCTCATCTGCACACT 1260
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 VERSION U94176.1
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 Papio hamadryas.
 Papio hamadryas
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 Cercopithecinae; Papio.
 REFERENCE 1 (bases 1 to 2769)
 AUTHORS Choong,C.S., Kempainen,J.A. and Wilson,E.M.
 TITLE Evolution of the primate androgen receptor: a structural basis for
 disease
 J. Mol. Evol. 47 (3), 334-342 (1998)
 MEDLINE 98404153
 PUBMED 9732460
 REFERENCE 2 (bases 1 to 2769)
 AUTHORS Choong,C.S., Kempainen,J.A. and Wilson,E.M.
 TITLE Direct Submission
 JOURNAL Submitted (18-MAR-1997) Laboratories for Reproductive Biology,
 University of North Carolina at Chapel Hill, CB 7500, MSRB, Rm 370,
 UNC-CH, Chapel Hill, NC 27599, USA
 FEATURES
 Location/Qualifiers
 1..2769
 source

us-09-497-822c-18.rge

Fri May 9 14:20:38 2003

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Search completed: May 8, 2003, 18:56:01
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